

## SEQUENCE LISTING

<110> BURNIE, JAMES PETER  
MATTHEWS, RUTH CHRISTINE

<120> MEDICAMENT

<130> 050885-0281578

<140> PCT/GB00/00237

<141> 2000-01-28

<140> GB 9902555.3

<141> 1999-02-05

<150> 09/889,314

<151> 2001-07-16

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 1491

<212> DNA

<213> Chlamydia pneumoniae

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<221> CDS

<222> (1)..(1491)

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aat atc atg tct caa gtt ctg aca tcg aca ccc cag ggc gtg ccc caa	96
Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln	
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caa gat aag ctg tct ggc aac gaa acg aag caa ata cag caa aca cgt	144
Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg	
35 40 45	
cag ggt aaa aac act gag atg gaa agc gat gcc act att gct ggt gct	192
Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala	
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tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca	240
Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro	
65 70 75 80	
caa cag gga gtt gct gct ggg aaa gaa tcc tca gaa agt caa aag gca	288
Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala	
85 90 95	

ggt gct gat act gga gta tca gga gcg gct gct act aca gca tca aat	336
Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn	
100 105 110	
act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa	384
Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys	
115 120 125	
agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa	432
Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln	
130 135 140	
atg aaa gaa gtc gaa gcg gtt gtt gtt gct gcc ctc tca ggg aaa agt	480
Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser	
145 150 155 160	
tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg	528
Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val	
165 170 175	
aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca	576
Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala	
180 185 190	
att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca	624
Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala	
195 200 205	
agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag	672
Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys	
210 215 220	
caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag	720
Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys	
225 230 235 240	
gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc	768
Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val	
245 250 255	
aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att	816
Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile	
260 265 270	
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Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala	
275 280 285	
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Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala	
290 295 300	
gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa	960
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305 310 315 320	

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325 330 335	
gct ata aaa gcg gct gtc aaa tct gga ata aaa gca ttt atc aaa act Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr	1056
340 345 350	
tta gtc aaa gcg att gcc aaa gcc att tct aaa gga atc tct aag gtt Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val	1104
355 360 365	
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370 375 380	
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385 390 395 400	
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405 410 415	
ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly	1296
420 425 430	
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435 440 445	
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450 455 460	
atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gcg tat Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr	1440
465 470 475 480	
gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe	1488
485 490 495	
taa	1491

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&lt;211&gt; 496

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 2

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Gln	Asp	Lys	Leu	Ser	Gly	Asn	Glu	Thr	Lys	Gln	Ile	Gln	Gln	Thr	Arg	
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Ser	Gly	Lys	Asp	Lys	Thr	Ser	Ser	Thr	Thr	Lys	Thr	Glu	Thr	Ala	Pro	
		65			70					75					80	
Gln	Gln	Gly	Val	Ala	Ala	Gly	Lys	Glu	Ser	Ser	Glu	Ser	Gln	Lys	Ala	
				85					90					95		
Gly	Ala	Asp	Thr	Gly	Val	Ser	Gly	Ala	Ala	Ala	Thr	Thr	Ala	Ser	Asn	
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Thr	Ala	Thr	Lys	Ile	Ala	Met	Gln	Thr	Ser	Ile	Glu	Glu	Ala	Ser	Lys	
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Ser	Met	Glu	Ser	Thr	Leu	Glu	Ser	Leu	Gln	Ser	Leu	Ser	Ala	Ala	Gln	
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Met	Lys	Glu	Val	Glu	Ala	Val	Val	Val	Ala	Ala	Leu	Ser	Gly	Lys	Ser	
					150					155					160	
Ser	Gly	Ser	Ala	Lys	Leu	Glu	Thr	Pro	Glu	Leu	Pro	Lys	Pro	Gly	Val	
				165					170					175		
Thr	Pro	Arg	Ser	Glu	Val	Ile	Glu	Ile	Gly	Leu	Ala	Leu	Ala	Lys	Ala	
			180					185					190			
Ile	Gln	Thr	Leu	Gly	Glu	Ala	Thr	Lys	Ser	Ala	Leu	Ser	Asn	Tyr	Ala	
							200					205				
Ser	Thr	Gln	Ala	Gln	Ala	Asp	Gln	Thr	Asn	Lys	Leu	Gly	Leu	Glu	Lys	
						215					220					
Gln	Ala	Ile	Lys	Ile	Asp	Lys	Glu	Arg	Glu	Glu	Tyr	Gln	Glu	Met	Lys	
					230					235					240	
Ala	Ala	Glu	Gln	Lys	Ser	Lys	Asp	Leu	Glu	Gly	Thr	Met	Asp	Thr	Val	
				245					250					255		
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			260					265					270			
Val	Ala	Ala	Ile	Phe	Thr	Cys	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Ala	Ala	
							280					285				
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						295					300					
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Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala  
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Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr  
340 345 350

Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val  
355 360 365

Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser  
370 375 380

Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly  
385 390 395 400

Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln  
405 410 415

Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly  
420 425 430

Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp  
435 440 445

Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu  
450 455 460

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Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe  
485 490 495

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Codon  
optimised N-terminal section of Chlamydia  
pneumoniae protein

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<222> (1)..(30)  
<223> S-tag and thrombin cleavage site

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<223> Positions (297)..(302) comprise Histidine tag

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 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala  
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 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro  
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 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala  
           210                          215                          220  
 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala  
           225                          230                          235                          240  
 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys  
                           245                          250                          255  
 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys  
           260                          265                          270  
 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val  
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